

Figure 1. The three primary components of the PIE. 1) The identification (inward) step locates putative genomic origin(s) for the sample. 2) The outward projection step predicts putative mature protein products that might originate from the locus found in step 1 using a breadth-first, heuristically-bounded search. 3) Each putative product is mapped through plug-in modules representing the separation and detection methods used, with Bayes statistics used to assign a probability score for the putative product based upon how well the artificial spectra match the details of the real spectra.

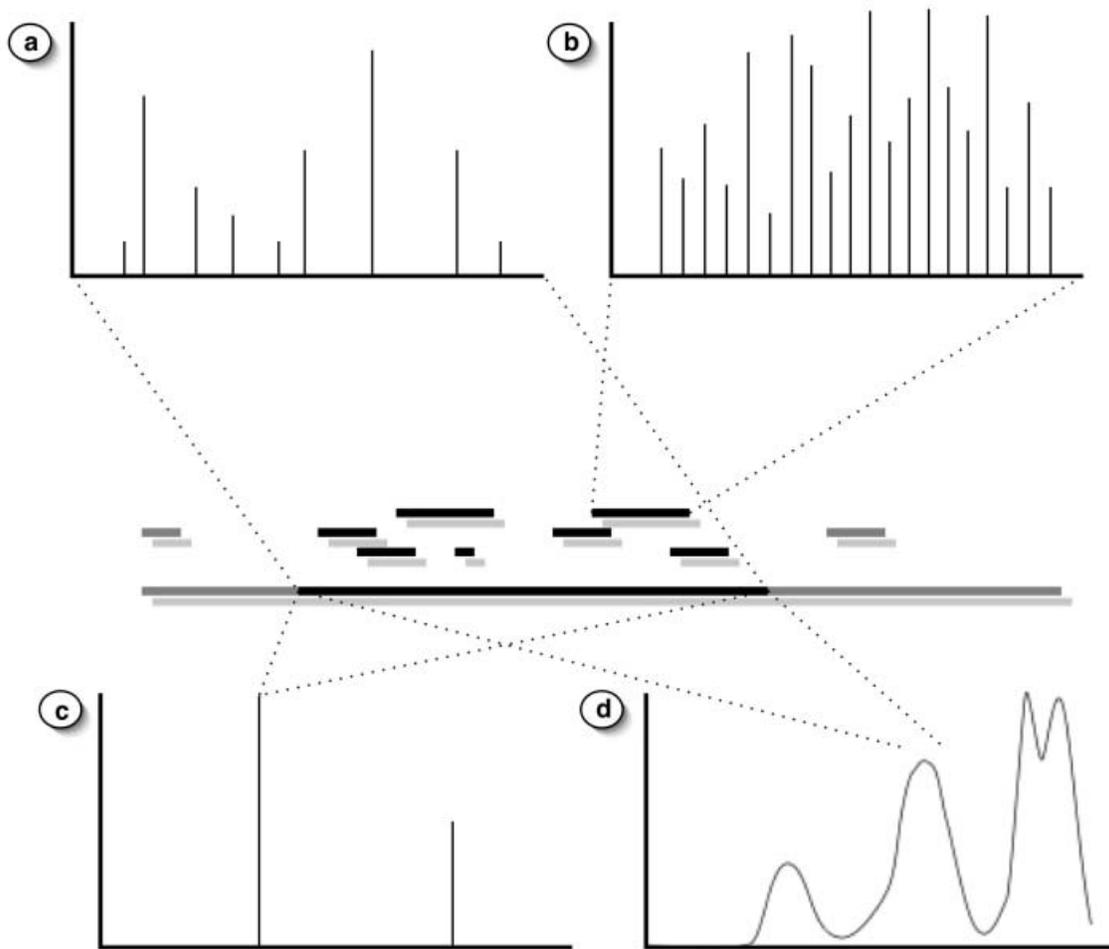


Figure 2. The outward-projection from a genomic region to mass spec data. The putative protein products of this sequence region can be matched against a variety of data collected in the laboratory, including a) peptide mass fingerprint, b) tandem mass spectra, c) intact mass measurements, d) LC profiles (UV).